

**Recruitment Effects In
Heterosexually Transmitted Disease Models**

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RECRUITMENT EFFECTS IN HETEROSEXUALLY TRANSMITTED DISEASE MODELS*

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Abstract:

We formulate and partially analyze a model for heterosexually transmitted diseases from which infecteds recover without partial or temporary immunity. We compute the threshold that determines the transition between disease-free and endemic equilibria as parameters are varied, and show that if recruitment of new susceptibles depends on disease prevalence then the endemic equilibrium may be unstable.

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1. Introduction

The history of models for sexually-transmitted diseases begins with the malaria model of Ross (1911, p.667), who recognized that vector- and sexually-transmitted diseases have equivalent mathematical formulations. In Ross' malaria model, transmission is through a female vector. Humans bitten by infected female mosquitoes may become infected and female mosquitoes may become infected by biting infected humans. Transmission from mosquitoes to mosquitoes or from humans to humans is not possible, except through blood transfusions. However, despite these similarities, vector-transmission takes place at a faster time scale. Because of the need for future theoretical work on models for vector-transmitted diseases (e.g. malaria infects and kills more individuals than all other diseases) we will outline the connection between vector- and heterosexually-transmitted diseases in the conclusion. We believe that the approaches that we use in this manuscript may be useful also in the study of the transmission dynamics of vector-transmitted diseases. The first model used for the explicit study of a sexually-transmitted disease, namely gonorrhea, was a one-sex model [Cooke and Yorke (1973)]. A two-sex model developed specifically for gonorrhea was formulated by Lajmanovich and Yorke (1976). Concerns with the HIV/AIDS epidemic have generated extensive research activity on models for the sexual-transmission of HIV/AIDS. However, most work has concentrated on the study on models for the homosexual transmission of HIV/AIDS [see Castillo-Chavez, (1989), Anderson and May (1991), Gabriel et al. (1990), Velasco-Hernandez and Hsieh (1993)]. For some notable exceptions see the work of Hoppensteadt (1974), Castillo-Chavez and Busenberg (1991), Castillo-Chavez et al. (1991), Dietz and Haderler (1988), Haderler (1989), Haderler and Nagoma (1990), Haderler et al. (1988), Waldstätter (1989), Schmitz et al. (1993).

In this paper we formulate and partially analyze models for the simplest possible heterosexually transmitted disease, namely a two-sex S-I-S model which would be appropriate for diseases without immunity such as gonorrhea. We incorporate epidemiological and demographic effects. These effects may be coupled or decoupled. Most models have usually assumed

that they are decoupled. Some exceptions, in the context of homosexually-transmitted diseases includes the work of Blythe et al. (1992), Scalia-Tomba (1991), Heiderich et al. (1993), and Haderler and Castillo-Chavez (1993).

In most population models, demographic effects may include births and deaths. For a sexually transmitted disease model it is reasonable to assume a mortality rate from causes unrelated to the disease (retirement from risky-sexual activity) but it is not appropriate to consider a birth rate, and hence we consider rates of recruitment into the heterosexually-active population under study. In fact, we study disease dynamics in a very simplified scenario, that is, we implicitly assume that most of the risky sexual activity takes place within the modeled population, the core group, and that the rate of sexual activity between core and non-core group members is negligible. This approach allows for the exploration of the effects of coupled demographic and epidemiological factors in as simple a setting as possible. The scenario that we have chosen is simple but realistic as there is considerable indication that the core group is the source for most cases of sexually transmitted diseases. For example, Hethcote and Yorke (1984) describe a gonorrhea model in which there is a core population forming 2% of the total population which contains 13% of the cases of disease and is responsible, through contacts with the non-core group, for 60% of the cases. We shall describe a model for the core group of the most sexually active members of a larger but unspecified population. The coupling between demographic and epidemiological effects is through the recruitment of new susceptibles as we are assuming that there is essentially no infection in the larger population. By looking at the disease only in the core group we lose some realism but we avoid the model complication of subdividing the population into risk classes depending on the level of sexual activity [Castillo-Chavez and Busenberg (1991)]. Thus we are able to get a better understanding of the role of behavior in core-disease dynamics by assuming that the recruitment rates into the core population depend on the size of the core population and by considering the possibility that potential recruits to the core population may be influenced by the prevalence of infection within the core. As we shall see, this will allow the possibility of instability and oscillation in the model.

2. A model for heterosexually transmitted diseases

We let S_f and S_m denote the number of susceptible females and males respectively. I_f and I_m the number of infective females and males respectively, and N_f and N_m the total female and male population sizes. As we are formulating an S-I-S model, with no immunity following recovery,

$$N_f = S_f + I_f, \quad N_m = S_m + I_m.$$

We shall describe the model in terms of the variables I_f, N_f, I_m , and N_m , but it will be convenient to use S_f and S_m in the description with the understanding that

$$S_f = N_f - I_f, \quad S_m = N_m - I_m.$$

Our model will involve two epidemiological processes – the acquisition of and recovery from infection. It will also involve two demographic processes – the recruitment of new members into core groups of females and males, and the deaths (retirement from risky sexual activity) of members. Thus there are four processes altogether, and we must make assumptions about each in order to construct our model.

We assume that there is a rate of recruitment of new members in each sex and a constant per capita death rate μ which is the same for both sexes, that is $1/\mu$ denotes the average period of sexual activity (the length of the average sexual-life). We are interested in the situation in which population sizes remain bounded in the absence of infection. Thus we assume that recruitment rates depend on total population size; the rate of recruitment of females is a function $F(N_f)$ and the rate of recruitment of new males is a function $M(N_m)$. Then, in the absence of infection the total population sizes for the two sexes satisfy

$$N'_f = F(N_f) - \mu N_f$$

$$N'_m = M(N_m) - \mu N_m.$$

We assume that there are carrying capacities K_f and K_m such that

$$F(K_f) = \mu K_f, \quad F'(K_f) < \mu, \quad F(N_f) > \mu N_f \quad (0 < N_f < K_f)$$

(1)

$$M(K_m) = \mu K_m, \quad M'(K_m) < \mu, \quad M(N_m) > \mu N_m \quad (0 < N_m < K_m)$$

When infection is present, we will assume that the per capita death rates are the same for infected and healthy members, that is, there is no disease-induced mortality.

Next, we describe the assumptions that we make on epidemiological effects, beginning with the assumptions on the rate of new infections.

We assume that the number of contacts capable of passing infection per male in unit time is a function $c_m(N_f)$ of the female population size, and that the number of contacts capable of passing infection per female in unit time is a function $c_f(N_m)$ of the male population size. Because the total number of such contacts in unit time by males must equal the total number of such contacts in unit time by females, we have the balance law

$$N_m c_m(N_f) = N_f c_f(N_m)$$

[Castillo-Chavez and Busenberg (1991)]. If we define

$$\hat{c}_m(N_f) = \frac{c_m(N_f)}{N_f}, \quad \hat{c}_f(N_m) = \frac{c_f(N_m)}{N_m},$$

the balance law takes the form

$$\hat{c}_m(N_f) = \hat{c}_f(N_m) \tag{2}$$

It is often assumed that the functions c_m and c_f are linear, so that $c_m(N_f) = \beta N_f$, $c_f(N_m) = \beta N_m$, and then the balance law becomes

$$\hat{c}_m(N_f) = \hat{c}_f(N_m) = \beta$$

We may generalize by allowing the possibility of saturation in contacts, and it is reasonable to assume that c_f and c_m are non-decreasing functions while \hat{c}_f and \hat{c}_m are non-increasing functions of the variables N_m and N_f respectively. Thus we assume

$$\begin{aligned} \hat{c}'_f(N_m) &\leq 0, \quad \hat{c}'_m(N_f) \leq 0 \\ [c_f(N_m)]' &= [N_m \hat{c}_f(N_m)]' = \hat{c}_f(N_m) + N_m \hat{c}'_f(N_m) \geq 0 \\ [c_m(N_f)]' &= [N_f \hat{c}_m(N_f)]' = \hat{c}_m(N_f) + N_f \hat{c}'_m(N_f) \geq 0 \end{aligned} \tag{3}$$

The number of new female infections in unit time is the number $c_m(N_f)$ of contacts per male multiplied by the number I_m of infective males multiplied by the probability S_f/N_f that the female contacted is not yet infected. Thus the rate of new female infections in unit time is

$$c_m(N_f)I_mS_f/N_f = \hat{c}_m(N_f)I_mS_f.$$

Similarly, the rate of new male infections in unit time is

$$\hat{c}_f(N_m)I_fS_m.$$

Our assumption on the rate of recovery from infection is that there is a non-increasing function $P_0(s)$, with $P_0(0) = 1$, describing the fraction of the members of each group who remain infective if still alive a time s after becoming infected. The two most-studied special cases in epidemiological modelling are

$$P_0(s) = e^{-\frac{1}{\tau_0}s},$$

which leads to ordinary differential equations models, and

$$P_0(s) = \begin{cases} 1, & 0 \leq s \leq \tau_0 \\ 0, & s > \tau_0, \end{cases}$$

which leads to differential-difference equation models. We formulate our model in terms of an arbitrary distribution of infective periods in order to study whether the qualitative behavior of the model depends on the form of $P_0(s)$.

The fraction of infectives remaining alive and infective a time s after becoming infected is

$$P(s) = e^{-\mu s} P_0(s). \tag{4}$$

The mean infective period (corrected for mortality) is

$$\tau = \int_0^\infty P(s)ds = \int_0^\infty e^{-\mu s} P_0(s)ds. \tag{5}$$

To simplify the exposition (we shall return to this point later), we assume that the rates of disease transmission per contact are independent of the gender of the infected individual. This is obviously not the case as it is well known that the probability of transmission per contact per infected male is larger than that for a female in the case of gonorrhea [see Hethcote and Yorke, (1984)] and drastically different for males and females in HIV-transmission [Padian and Jewell, (1991)].

With the above hypotheses on the rates of acquisition of and recovery from infection and the rates of recruitment and mortality, our model is given by the system.

$$\begin{aligned} I_f(t) &= \int_{-\infty}^t \hat{c}_m(N_f(x)) S_f(x) I_m(x) P(t-x) dx \\ N_f' &= F(N_f) - \mu N_f \\ I_m(t) &= \int_{-\infty}^t \hat{c}_f(N_m(x)) S_m(x) I_f(x) P(t-x) dx \\ N_m' &= M(N_m) - \mu N_m \end{aligned} \tag{6}$$

Equilibria (constant solutions) of (6) are solutions of the two pairs of equations

$$I_f = \hat{c}_m(N_f) \tau S_f I_m, I_m = \hat{c}_f(N_m) \tau S_m I_f \tag{7}$$

$$F(N_f) = \mu N_f, M(N_m) = \mu N_m \tag{8}$$

It follows from (8) that $N_f = K_f, N_m = K_m$. The balance law (2) gives

$$\hat{c}_m(N_f) = \hat{c}_f(N_m)$$

and we define

$$\beta = \hat{c}_m(K_f) = \hat{c}_f(K_m).$$

Then (7) becomes

$$I_f = \beta \tau S_f I_m, I_m = \beta \tau S_m I_f \tag{9}$$

If $I_f = 0$ then $I_m = 0$ and it follows that $S_f = K_f, S_m = K_m$ (disease-free equilibrium). On the other hand, if $I_f > 0$, then (9) gives

$$\frac{I_f}{S_f I_m} = \frac{I_m}{S_m I_f} = \beta \tau,$$

which implies

$$\frac{I_m^2}{S_m} = \frac{I_f^2}{S_f}.$$

Because

$$(\beta\tau)^2 S_f S_m = 1 \quad (10)$$

if $I_f > 0, I_m > 0$, the existence of an endemic equilibrium (an equilibrium with $I_f > 0, I_m > 0, 0 \leq S_f < K_f, 0 \leq S_m < K_m$) requires

$$(\beta\tau)^2 K_f K_m > 1.$$

In fact, if $(\beta\tau)^2 K_f K_m > 1$, we may solve (9) by elimination, using $S_f = K_f - I_f, S_m = K_m - I_m$, to obtain the unique endemic equilibrium

$$\begin{aligned} I_f &= \frac{(\beta\tau)^2 K_m K_f - 1}{\beta\tau(\beta\tau K_m + 1)}, S_f = \frac{\beta\tau K_f + 1}{\beta\tau(\beta\tau K_m + 1)}, N_f = K_f \\ I_m &= \frac{(\beta\tau)^2 K_m K_f - 1}{\beta\tau(\beta\tau K_f + 1)}, S_m = \frac{\beta\tau K_m + 1}{\beta\tau(\beta\tau K_f + 1)}, N_m = K_m \end{aligned} \quad (11)$$

The linearization of the system (6) at an equilibrium (I_f, N_f, I_m, N_m) is

$$\begin{aligned} u_f(t) &= \int_{-\infty}^t [-I_m \hat{c}_m(N_f) u_f(x) + I_m \{\hat{c}_m(N_f) + S_f \hat{c}'_m(N_f)\} v_f(x) + \hat{c}_m(N_f) S_f U_m(x)] P(t-x) dx \\ v'_f &= [F'(N_f) - \mu] v_f \\ u_m(t) &= \int_{-\infty}^t [\hat{c}_f(N_m) S_m u_f(x) - I_f \hat{c}_f(N_m) u_m(x) + I_f \{\hat{c}_f(N_m) + S_m \hat{c}'_f(N_m)\} v_m(x)] P(t-x) ds \\ v'_m &= [M'(N_m) - \mu] v_m \end{aligned}$$

The characteristic equation (the condition that this linearization have a solution whose components are constant multiples of $e^{\lambda t}$) is

$$\det \begin{bmatrix} -\hat{c}_m(N_f) I_m \hat{P}(\lambda) - 1 & I_m Q_f(N_f) \hat{P}(\lambda) & S_f \hat{c}_m(N_f) \hat{P}(\lambda) & 0 \\ 0 & F'(N_f) - \mu - \lambda & 0 & 0 \\ S_m \hat{c}_f(N_m) \hat{P}(\lambda) & 0 & -\hat{c}_f(N_m) I_f \hat{P}(\lambda - 1) & I_f Q_m(N_m) \hat{P}(\lambda) \\ 0 & 0 & 0 & M'(N_m) - \mu - \lambda \end{bmatrix} = 0 \quad (12)$$

where

$$\hat{P}(\lambda) = \int_0^\infty e^{-\lambda s} P(s) ds,$$

the Laplace transform of $P(s)$, and

$$\hat{P}(0) = \int_0^\infty P(s) ds = \tau,$$

and

$$\begin{aligned} Q_f(N_f) &= \hat{c}_m(N_f) + S_f \hat{c}'_m(N_f) \\ Q_m(N_m) &= \hat{c}_f(N_m) + S_m \hat{c}'_f(N_m) \end{aligned}$$

Because $\hat{c}'_m(N_f) \leq 0, S_f \leq N_f$, we have

$$Q_f(N_f) \geq \hat{c}_m(N_f) + N_f \hat{c}'_m(N_f) = c'_m(N_f) \geq 0$$

and similarly $Q_m(N_m) \geq 0$. An equilibrium is asymptotically stable if and only if all roots of the characteristic equation at the equilibrium have negative real part (see, for example [Webb (1985), Chapter 5]). At the disease-free equilibrium, $I_f = 0, I_m = 0, S_f = N_f = K_f, S_m = N_m = K_m$, and the characteristic equation is

$$[F'(K_f) - \mu - \lambda][M'(K_m) - \mu - \lambda][\beta^2 K_m K_f \{\hat{P}(\lambda)\}^2 - 1] = 0$$

Because of (1) the roots of the characteristic equation are the negative real roots $F'(K_f) - \mu$ and $M'(K_m) - \mu$ together with the roots of

$$\beta^2 K_m K_f \{\hat{P}_1(\lambda)\}^2 = 1.$$

Because

$$\beta^2 K_m K_f [\hat{P}(\lambda)]^2 \leq \beta^2 K_m K_f |\hat{P}(0)|^2 = \beta^2 K_f K_m \tau^2$$

for $\text{Re} \lambda \geq 0$ there can be no root of the characteristic equation with non-negative real part if $\beta^2 K_f K_m \tau^2 < 1$. In fact, it is not difficult to see that the condition

$$\beta^2 K_f K_m \tau^2 < 1$$

is necessary and sufficient for the asymptotic stability of the disease-free equilibrium. The basic reproductive number for the model (6) is

$$R_0 = \beta\tau\sqrt{K_f K_m}$$

and we see that the disease-free equilibrium is asymptotically stable if and only if $R_0 < 1$. It is not difficult to show by standard methods involving a priori estimates that the asymptotic stability is global if $R_0 < 1$.

If $R_0 > 1$, so that the disease-free equilibrium is unstable, there is a unique endemic equilibrium and the characteristic equation at this equilibrium (after removal of the factors $[F'(K_f) - \mu - \lambda][M'(K_m) - \mu - \lambda]$) is

$$\beta^2(S_f S_m - I_f I_m)[\hat{P}(\lambda)]^2 - \beta(I_m + I_f)\hat{P}(\lambda) - 1 = 0,$$

which we may solve for $\hat{P}(\lambda)$ to obtain

$$\hat{P}(\lambda) = \frac{\beta(I_m + I_f) \pm \sqrt{\beta^2(I_m + I_f)^2 + 4(S_f S_m - I_f I_m)}}{2\beta^2(S_f S_m - I_f I_m)}. \quad (13)$$

Thus the characteristic equation splits into two equations

$$\hat{P}(\lambda) = a, \quad \hat{P}(\lambda) = b.$$

Because

$$\beta^2(I_m + I_f)^2 + 4(S_f S_m - I_f I_m) = \beta^2(I_m - I_f)^2 + 4S_f S_m \geq 0,$$

both a and b are real. If $S_f S_m - I_f I_m > 0$, then $b < 0$ but $a > 0$, while if $S_f S_m - I_f I_m < 0$, then both a and b are negative. It is known [Brauer (1987)] that all roots of a characteristic equation $\hat{P}(\lambda) = a$ have negative real part if and only if $\hat{P}(0)/a < 1$. In particular, if $a < 0$ then all roots of $\hat{P}(\lambda) = a$ have negative real part. Thus the only possibility for a root of (13) with non-negative real part is if $S_f S_m - I_f I_m > 0$ with the factor

$$\hat{P}(\lambda) = a = \frac{\beta(I_m + I_f) + \sqrt{\beta^2(I_m - I_f)^2 + 4\beta^2 S_f S_m}}{2\beta^2(S_f S_m - I_f I_m)}.$$

But

$$a > \frac{2\beta\sqrt{S_f S_m}}{2\beta^2 S_f S_m} = \frac{1}{\beta\sqrt{S_f S_m}} = \tau$$

by (10), and the stability condition $\hat{P}(0)/a < 1$ is satisfied because $\hat{P}(0) = \tau$.

We have now established the following result:

THEOREM 1: Under the hypotheses (1), (3), (4), (5), the model (6) with $S_f + I_f = N_f$, $S_m + I_m = N_m$ has a disease-free equilibrium $S_f = K_f$, $S_m = K_m$, $I_f = 0$, $I_m = 0$ which is globally asymptotically stable if $R_0 = \beta\tau\sqrt{K_f K_m} < 1$. If $R_0 > 1$, the disease-free equilibrium is unstable but there is an endemic equilibrium with $S_f < K_f$, $S_m < K_m$, $I_f > 0$, $I_m > 0$ given by (11) which is asymptotically stable.

In formulating the model (6), we have assumed that the probabilities of transmission of infection from male to female and from female to male are the same. If this is not true, we would assume that the rate of new female infections in unit time is $p\hat{c}_m(N_f)I_m S_f$ and that the rate of new male infections in unit time is $q\hat{c}_m(N_f)I_m S_f$ with $p \neq q$. The integral equations in the model (6) would then be replaced by

$$I_f(t) = \int_{-\infty}^t p\hat{c}_m(N_f(x))S_f(x)I_m(x)P(t-x)dx$$

$$I_m(t) = \int_{-\infty}^t q\hat{c}_f(N_m(x))S_m(x)I_f(x)P(t-x)dx.$$

The equilibrium conditions would become

$$I_f = p\beta\tau S_f I_m, \quad I_m = q\beta\tau S_m I_f,$$

which imply $pq(\beta\tau)^2 S_f S_m = 1$. The characteristic equation at an equilibrium now reduces to

$$\det \begin{bmatrix} -p\beta I_m \hat{P}(\lambda) - 1 & p\beta S_f \hat{P}(\lambda) \\ q\beta S_m \hat{P}(\lambda) & -\beta q I_f \hat{P}(\lambda) - 1 \end{bmatrix} = 0.$$

At the disease-free equilibrium, the characteristic equation is

$$pq\beta^2 K_m K_f [\hat{P}(\lambda)]^2 = 1$$

and the necessary and sufficient condition for asymptotic stability is

$$R_0 = \beta\tau\sqrt{pqK_mK_f} < 1.$$

The analysis for the endemic equilibrium is analogous to that when $p = q = 1$, and we find that the endemic equilibrium is asymptotically stable if $R_0 > 1$. Thus the results are completely analogous to those in the case of equal disease transmission probabilities. Hence asymmetric transmission probabilities will lead to the same qualitative dynamics. The potential dynamics if one considers a fatal sexually-transmitted disease such as HIV/AIDS are poorly understood. For example, if one considers a one-sex two-group epidemiological model for a fatal sexually-transmitted disease, we observe that pronounced asymmetry in epidemiological parameters implies the possibility of multiple endemic equilibria (see Castillo-Chavez et al. 1989, Huang et al. 1992).

3. Recruitment depending on disease status

If the recruitment functions F and M depend on the size of the infective populations as well as on total population sizes, the analysis is considerably more complicated. We now let $F(I_f, N_f)$ be the rate of recruitment of females in unit time and $M(I_m, N_m)$ the rate of recruitment of males in unit time. In the model (6) we replace $F(N_f)$ by $F(I_f, N_f)$ and $M(N_m)$ by $M(I_m, N_m)$. It is reasonable to assume that the recruitment rates decrease as the number of infectives increase, so that

$$F_I(I_f, N_f) < 0, \quad M_I(I_m, N_m) < 0. \quad (14)$$

Two special cases of interest are recruitment function of the form

$$F(I, N) = G_1(I), \quad G'_1(I) < 0$$

so that $F_I(I, N) < 0$, $F_N(I, N) \equiv 0$, and

$$F(I, N) = G_2(I/N), \quad G'_2(P) < 0$$

so that $F_I(I, N) < 0$, $F_N(I, N) > 0$ and $IF_I(I, N) + NF_N(I, N) \equiv 0$. To locate equilibria of the model (6) we must consider a curve of the form $y = F(I, N)$ with I as a parameter. This curve for $I = 0$ is assumed to intersect the line $y = \mu N$ when $N = K$ if $I = 0$, and it is assumed that $F(0, N) > \mu N$ for $0 < N < K$, $F_N(0, N) < \mu$. If $F_I(I, N) < 0$, then the curve $y = F(I, N)$ moves down as I increases and intersects the line $y = \mu N$ for $N = N(I) < K$. We assume $F(I, N) > \mu N$ for $0 < N < N(I)$, $F_N(I, N(I)) < \mu$.

Equilibria of (6) are given by

$$F(I_f, N_f) = \mu N_f, \quad M(I_m, N_m) = \mu N_m$$

and (7), and we are assuming that at an equilibrium (I_f, N_f, I_m, N_m) we have

$$F_N(I_f, N_f) < \mu, \quad M_N(I_m, N_m) < \mu. \quad (15)$$

The characteristic equation at an equilibrium is now given by the determinant of the matrix

$$\begin{bmatrix} -\hat{c}_m(N_f)I_m\hat{P}(\lambda) - 1 & I_mQ_f(N_f)\hat{P}(\lambda) & S_f\hat{c}_m(N_f)\hat{P}(\lambda) & 0 \\ F_I(I_f, N_f) & F_N(I_f, N_f) - \mu - \lambda & 0 & 0 \\ S_m\hat{c}_f(N_m)\hat{P}(\lambda) & 0 & -\hat{c}_f(N_m)I_f\hat{P}(\lambda) - 1 & I_f(Q_m(N_m)\hat{P}(\lambda) \\ 0 & 0 & M_I(I_m, N_m) & M_N(I_m, N_m) - \mu - \lambda \end{bmatrix}$$

equal to zero. Because of the entries $F_I(I_f, N_f)$ and $M_I(I_m, N_m)$ we can no longer remove the factors $F_N(I_f, N_f) - \mu - \lambda$ and $M_N(I_m, N_m) - \mu - \lambda$ as we did in analyzing (12). At the disease-free equilibrium, because $I_m = 0$, $I_f = 0$ the characteristic equation reduces just as before and this equilibrium is asymptotically stable if and only if $R_0 < 1$.

At the endemic equilibrium, the characteristic equation is

$$\left[1 + \beta I_m \hat{P}(\lambda) - \frac{F_I(I_f, N_f) I_m Q_f(N_f) \hat{P}(\lambda)}{\lambda + \mu - F_N(I_f, N_f)} \right] \cdot \quad (16)$$

$$\left[1 + \beta I_f \hat{P}(\lambda) - \frac{M_I(I_m, N_m) I_f Q_m(N_m) \hat{P}(\lambda)}{\lambda + \mu - M_N(I_m, N_m)} \right] = \hat{c}_f(N_m) \hat{c}_m(N_f) S_f S_m \left[\hat{P}(\lambda) \right]^2.$$

We let

$$\begin{aligned}\lambda_f &= \mu - F_N(I_f, N_f), \quad \lambda_m = \mu - M_N(I_m, N_m) \\ p_f &= -F_I(I_f, N_f)I_m Q_f(N_f), \quad p_m = -M_I(I_m, N_m)I_f Q_m(N_m) \\ q_f &= \beta I_m, \quad q_m = \beta I_f.\end{aligned}$$

Then the assumptions (14), (15) imply

$$\lambda_f > 0, \lambda_m > 0, p_f > 0, p_m > 0, q_f > 0, q_m > 0. \quad (17)$$

Writing (16) in terms of these parameters and making use of (10), we may write the characteristic equation at an endemic equilibrium as

$$\left[1 + q_f \hat{P}(\lambda) + \frac{p_f \hat{P}(\lambda)}{\lambda + \lambda_f}\right] \left[1 + q_m \hat{P}(\lambda) + \frac{p_m \hat{P}(\lambda)}{\lambda + \lambda_m}\right] = \frac{[\hat{P}(\lambda)]^2}{\tau^2}. \quad (18)$$

We are unable to analyze the characteristic equation (18) in general, but we can treat some special cases.

Let us consider the case of exponentially distributed infective periods, where the model (6) reduces to a system of ordinary differential equations. We use

$$P_0(s) = e^{-s/\tau_0}, \quad P(s) = e^{-(\mu + \frac{1}{\tau_0})s},$$

so that $\tau = \frac{\tau_0}{\mu\tau_0 + 1}$. If we write $a = 1/\tau$, then $P(s) = e^{-as}$, $\hat{P}(0) = 1/a$, $\hat{P}(\lambda) = \frac{1}{\lambda + a}$. The characteristic equation is then a fourth degree polynomial equation

$$[(\lambda + a)(\lambda + \lambda_f) + q_f(\lambda + \lambda_f) + p_f][(\lambda + a)(\lambda + \lambda_m) + q_m(\lambda + \lambda_m) + p_m] = a^2(\lambda + \lambda_f)(\lambda + \lambda_m).$$

This has the form

$$\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0$$

with

$$\begin{aligned}a_1 &= 2a + q_f + \lambda_f + q_m + \lambda_m \\ a_2 &= \lambda_f(a + q_f) + p_f + \lambda_m(a + q_m) + p_m + (a + q_f + \lambda_f)(a + q_m + \lambda_m) - a^2 \\ a_3 &= [\lambda_f(a + q_f) + p_f](a + q_m + \lambda_m) + [\lambda_m(a + q_m) + p_m](a + q_f + \lambda_f) - a^2(\lambda_f + \lambda_m), \\ a_4 &= [\lambda_f(a + q_f) + p_f][\lambda_m(a + q_m) + p_m] - a^2\lambda_m\lambda_f.\end{aligned}$$

Using (17) we can show by some tedious calculations that the Routh-Hurwitz conditions

$$a_1 > 0, a_4 > 0, \quad a_1 a_2 - a_3 > 0,$$

$$a_1 a_2 a_3 - a_1^2 a_4 - a_3^2 > 0$$

are satisfied. This shows that in the special case of exponentially distributed infective periods the endemic equilibrium is always asymptotically stable.

There are, however, situations in which the endemic equilibrium could be unstable. A specific example is easily obtained by considering the “symmetric” case in which F and M are the same function, $I_m = I_f$, and $c_m(N_f) = \beta N_f$, $c_f(N_m) = \beta N_m$ so that $\hat{c}_m(N_f) = \hat{c}_f(N_m) = \beta$ and $Q_f(N_f) = Q_m(N_m) = \beta$. The characteristic equation then becomes

$$\left[1 + q\hat{P}(\lambda) + \frac{p\hat{P}(\lambda)}{\lambda + \lambda_1} \right]^2 = \frac{[\hat{P}(\lambda)]^2}{\tau^2},$$

with $q = q_f = q_m$, $p = p_f = p_m$, $\lambda_1 = \lambda_f = \lambda_m$. We specialize further by taking $q = 1/\tau$, so that $I = S$. The characteristic equation factors,

$$\left[1 + \frac{p\hat{P}(\lambda)}{\lambda + \lambda_1} \right] \left[1 + \frac{p\hat{P}(\lambda)}{\lambda + \lambda_1} + 2q\hat{P}(\lambda) \right] = 0$$

and we will demonstrate the possibility of a root with non-negative real part of

$$1 + \frac{p\hat{P}(\lambda)}{\lambda + \lambda_1} = 0,$$

or

$$\lambda + \lambda_1 + p\hat{P}(\lambda) = 0. \tag{19}$$

To accomplish this, it suffices to show the possibility of a pure imaginary root $\lambda = iy$ with $y > 0$ of (19), and this is equivalent to the solvability of the pair of equations corresponding to the real and imaginary parts of (19),

$$\begin{aligned} p \int_0^\infty P(s) \cos y s ds + \lambda_1 &= 0, \\ p \int_0^\infty P(s) \sin y s ds - y &= 0. \end{aligned} \tag{20}$$

We take $\mu = 0$, so that $\lambda_1 = -F_N(I, N) > 0$, and choose

$$P(s) = \begin{cases} 1, & 0 \leq s \leq \tau \\ 0, & s > \tau \end{cases}$$

Then

$$\int_0^\infty P(s) \cos y s ds = \frac{\sin y \tau}{y}, \quad \int_0^\infty P(s) \sin y s ds = \frac{1 - \cos y \tau}{y}$$

and (20) becomes

$$\sin y \tau = -\lambda_1 y / p, \quad \cos y \tau = 1 - \frac{y^2}{p}.$$

We must have $\sin^2 y \tau + \cos^2 y \tau = 1$, and this implies the condition

$$y^2 = 2p - \lambda_1^2.$$

Thus we must choose λ_1 and p with $\lambda_1^2 < 2p$, and then we need to choose τ so that

$$\begin{aligned} \sin \tau \sqrt{2p - \lambda_1^2} &= -\lambda_1 \sqrt{2p - \lambda_1^2} / p \\ \cos \tau \sqrt{2p - \lambda_1^2} &= 1 - (2p - \lambda_1^2) / p = \lambda_1^2 / p - 1, . \end{aligned}$$

This is possible provided the values $-\lambda_1 \sqrt{2p - \lambda_1^2} / p$ and $\lambda_1^2 / p - 1$ of the trigonometric functions have absolute value no greater than 1, a consequence of $\lambda_1^2 < 2p$. Thus the endemic equilibrium is unstable for suitable choices of parameters in this example.

We conclude that when recruitment depends on disease state, instability of the endemic equilibrium is possible although not for exponentially distributed infective periods. As the instability is signalled by a pure imaginary root of the characteristic equation, we would expect a Hopf bifurcation and sustained oscillations about the endemic equilibrium.

4. Conclusions

In this work we have formulated a model for a heterosexually transmitted disease of S-I-S type. The formulation of S-I-R models with permanent removal or with recovery with immunity should be straightforward but the dynamics may be quite different. We have also considered the effect of demographic recruitment which depends on the number of infectives. This has not yet been studied thoroughly for models with direct transmission, although it is known that instability is possible for an S-I-R model with permanent removal even with exponentially distributed infective periods [Blythe, Brauer and Castillo-Chavez (1992)]. Our results here support a conjecture that in general recruitment depending on disease status tends to support the possibility of instability of equilibrium and oscillation. As our example of instability was essentially a one-sex model, we have no indication whether heterosexual S-I-S transmission models have qualitatively different behavior from direct transmission one-sex S-I-S models.

A full analysis of models with recruitment depending on disease state is indicated because it would have applications beyond sexually transmitted diseases. Models in which the demographic processes are births and deaths and in which there are births in both susceptible and infective classes, with birth rates which depend on the size of the infective class can describe diseases with vertical transmission [Busenberg and Cooke (1993)]. Both direct transmission (analogous to a one-sex model) and transmission through a vector (analogous to a two-sex model) are possible. As vertical transmission occurs in some diseases with millions of victims, there are many important questions. Most of the results known for vertical transmission are for models in which total population size would grow exponentially in the absence of disease. The corresponding results for populations with finite carrying capacity would be of great interest.

Although the generalization to S-I-R models with permanent removal or with recovery with immunity is straightforward, this is not quite the case if one wishes to extend these models to study the dynamics of vector-transmitted diseases.

As mentioned in the introduction, models of sexually-transmitted diseases (two-sexes) and vector-transmitted diseases have an analogous contact structure and both satisfy a conservation of contacts law. However, in vector-transmitted diseases there exists a fundamental asymmetry in the interaction because vectors choose hosts actively while hosts do not choose their vectors. This asymmetry may be modeled through the following modification of the balance law:

$$N_m c_m(N_m) = N_h c_h(N_m, N_h). \quad (21)$$

where h stands for hosts and m for vectors, and the contact rate per vector in unit time is a function of the vector population density while the host contact rate is a function of vector and host densities

The classical Ross-Macdonald model for malaria states that the transmission rate of *Plasmodium* from vector to host is a function of the biting rate of the mosquito and the ratio of vector numbers to host numbers. Therefore we have

$$c_m(N_m) I_m S_h / N_h \quad (22)$$

as the following expression for the host incidence rate. By taking

$$c_m(N_m) = \beta N_m$$

and substituting back into (22) we obtain the expression for the incidence rate in the Ross-Macdonald model:

$$c_m(N_m) I_m S_h / N_h = \beta \frac{N_m}{N_h} I_m S_h.$$

But (21) forces us to define

$$c_h(N_m) = N_m \left[\beta \frac{N_m}{N_h} \right]$$

which gives the following expression for the vector incidence:

$$c_h(N_m) I_h S_m / N_m = \beta \frac{N_m}{N_h} I_h S_m.$$

The last expression is in sharp contrast with the classical Ross-Macdonald model incidence rate,

$$\alpha I_h S_m$$

where α is a constant. Therefore, Ross-Macdonald-type models do not satisfy the balance law (21) unless N_m and N_h are constant and α (the fraction of the biting rate that results in infection in the vector) is proportional to β (the fraction of the biting rate that results in infection in the host). This last assumption must be weakened and incorporated into models with the above incidence rates. These studies may lead to our further understanding of vector-transmitted diseases.

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